

RAW SEQUENCE LISTING

DATE: 07/25/2001

PATENT APPLICATION: US/09/509,449C

TIME: 15:32:54

Input Set : A:\594-352SeqLst.txt

Output Set: N:\CRF3\07252001\I509449C.raw

ENTERED

3 <110> APPLICANT: Aoyagi, Katsumi
 4 Ohue, Chiharu
 5 Iida, Kumiko
 6 Yagi, Shintaro
 8 <120> TITLE OF INVENTION: METHOD FOR MEASUREMENT OF HEPATITIS C VIRUS
 10 <130> FILE REFERENCE: 594.352USWO
 12 <140> CURRENT APPLICATION NUMBER: US 09/509,449C
 13 <141> CURRENT FILING DATE: 2000-03-28
 15 <150> PRIOR APPLICATION NUMBER: JP 10-216094
 16 <151> PRIOR FILING DATE: 1998-07-30
 18 <150> PRIOR APPLICATION NUMBER: PCT/JP99/04129
 19 <151> PRIOR FILING DATE: 1999-07-30
 21 <160> NUMBER OF SEQ ID NOS: 11
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 177
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Hepatitis C virus
 30 <400> SEQUENCE: 1
 32 Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Pro Glu
 33 1 5 10 15
 36 Phe Met Gly Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr
 37 20 25 30
 40 Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val
 41 35 40 45
 44 Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg
 45 50 55 60
 48 Ala Thr Arg Lys Thr Ser Lys Arg Ser Gln Pro Arg Gly Gly Arg Arg
 49 65 70 75 80
 52 Pro Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly Lys Pro
 53 85 90 95
 56 Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly
 57 100 105 110
 60 Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp
 61 115 120 125
 64 Pro Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu Thr
 65 130 135 140
 68 Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Phe Arg Val Gly Ala Phe
 69 145 150 155 160
 72 Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu
 73 165 170 175
 76 Asp
 80 <210> SEQ ID NO: 2
 81 <211> LENGTH: 160
 82 <212> TYPE: PRT
 83 <213> ORGANISM: Hepatitis C virus
 85 <400> SEQUENCE: 2

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87 Met Gly Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
88 1      5      10      15
91 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
92      20      25      30
95 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
96      35      40      45
99 Thr Arg Lys Thr Ser Lys Arg Ser Gln Pro Arg Gly Gly Arg Arg Pro
100     50     55     60
103 Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly
104 65      70      75      80
107 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
108      85      90      95
111 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
112      100     105     110
115 Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu Thr Cys
116      115     120     125
119 Gly Phe Ala Asp Leu Met Gly Tyr Ile Phe Arg Val Gly Ala Phe Leu
120      130     135     140
123 Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
124 145      150     155     160
127 <210> SEQ ID NO: 3
128 <211> LENGTH: 20
129 <212> TYPE: PRT
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: Fused polypeptide including Hepatitis C virus sequence.
135 <400> SEQUENCE: 3
137 Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu
138 1      5      10      15
141 Leu Pro Arg Arg
142      20
145 <210> SEQ ID NO: 4
146 <211> LENGTH: 10
147 <212> TYPE: PRT
148 <213> ORGANISM: Artificial Sequence
150 <220> FEATURE:
151 <223> OTHER INFORMATION: Fused polypeptide including Hepatitis C virus sequence.
153 <400> SEQUENCE: 4
155 Gly Pro Arg Leu Gly Val Arg Ala Thr Arg
156 1      5      10
159 <210> SEQ ID NO: 5
160 <211> LENGTH: 21
161 <212> TYPE: PRT
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: Fused polypeptide including Hepatitis C virus sequence.
167 <400> SEQUENCE: 5
169 Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro Arg His Arg
170 1      5      10      15

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173 Ser Arg Asn Val Gly
 174 20
 177 <210> SEQ ID NO: 6
 178 <211> LENGTH: 20
 179 <212> TYPE: PRT
 180 <213> ORGANISM: Artificial Sequence
 182 <220> FEATURE:
 183 <223> OTHER INFORMATION: Fused polypeptide including Hepatitis C virus sequence.
 185 <400> SEQUENCE: 6
 187 Asp Pro Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu
 188 1 5 10 15
 191 Thr Cys Gly Phe
 192 20
 195 <210> SEQ ID NO: 7
 196 <211> LENGTH: 24
 197 <212> TYPE: DNA
 198 <213> ORGANISM: Artificial Sequence
 200 <220> FEATURE:
 201 <223> OTHER INFORMATION: Primer for polymerase chain reaction.
 203 <400> SEQUENCE: 7
 204 gaattcatgg gcacgaatcc taaa
 207 <210> SEQ ID NO: 8 24
 208 <211> LENGTH: 21
 209 <212> TYPE: DNA
 210 <213> ORGANISM: Artificial Sequence
 212 <220> FEATURE:
 213 <223> OTHER INFORMATION: Primer for polymerase chain reaction.
 215 <400> SEQUENCE: 8
 216 ttagtcctcc agaaccgga c
 219 <210> SEQ ID NO: 9 21
 220 <211> LENGTH: 16
 221 <212> TYPE: PRT
 222 <213> ORGANISM: Artificial Sequence
 224 <220> FEATURE:
 225 <223> OTHER INFORMATION: Portion of Hepatitis C virus sequence.
 227 <400> SEQUENCE: 9
 229 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile
 230 1 5 10 15
 233 <210> SEQ ID NO: 10
 234 <211> LENGTH: 1197
 235 <212> TYPE: DNA
 236 <213> ORGANISM: Artificial Sequence
 238 <220> FEATURE:
 239 <223> OTHER INFORMATION: Nucleotide sequence coding for chimeric antigen.
 241 <220> FEATURE:
 242 <221> NAME/KEY: CDS
 243 <222> LOCATION: (1)..(1188)
 244 <223> OTHER INFORMATION:
 247 <400> SEQUENCE: 10

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248	gaa	ttc	acc	aaa	gtg	ccg	ggt	gct	tat	gcg	gcc	aaa	ggt	tat	aag	gtc	48
249	Glu	Phe	Thr	Lys	Val	Pro	Val	Ala	Tyr	Ala	Ala	Lys	Gly	Tyr	Lys	Val	
250	1			5						10					15		
252	ctg	ggt	ctg	gac	ccg	agc	ggt	gcc	agc	acc	ctg	ggt	ttc	ggc	gcg	tat	96
253	Leu	Val	Leu	Asp	Pro	Ser	Val	Ala	Ser	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	
254				20					25					30			
256	ctg	agc	aag	gcc	cat	ggt	gtg	aac	ccg	aac	atc	cgc	acg	ggc	atc	cgt	144
257	Leu	Ser	Lys	Ala	His	Gly	Val	Asn	Pro	Asn	Ile	Arg	Thr	Gly	Ile	Arg	
258			35					40					45				
260	acc	ggt	acc	acc	ggt	gct	ccg	gtg	acc	tat	tcc	acc	tac	ggt	aaa	tac	192
261	Thr	Val	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Tyr	
262			50					55					60				
264	ctg	gcg	gac	ggc	ggt	tgc	gcc	ggc	ggt	gcg	tac	gat	gtg	atc	gga	tct	240
265	Leu	Ala	Asp	Gly	Gly	Cys	Ala	Gly	Gly	Ala	Tyr	Asp	Val	Ile	Gly	Ser	
266	65					70					75					80	
268	gga	gag	gag	gtg	gcc	ctg	tct	aac	act	gga	gag	gtc	ccc	ttc	tat	ggc	288
269	Gly	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Val	Pro	Phe	Tyr	Gly	
270				85					90					95			
272	cgc	gcg	atc	ccg	atc	gaa	gcg	atc	aaa	ggc	ggt	cgc	cat	ctg	ggt	ttc	336
273	Arg	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Lys	Gly	Gly	Arg	His	Leu	Val	Phe	
274				100					105					110			
276	tgc	cat	agc	aag	gag	aaa	tgc	gat	gaa	ctg	gcg	agc	gcg	ctg	tcc	gga	384
277	Cys	His	Ser	Lys	Glu	Lys	Cys	Asp	Glu	Leu	Ala	Ser	Ala	Leu	Ser	Gly	
278			115					120					125				
280	ttg	ggt	ctg	aac	gct	gtg	gca	ttc	tat	cgc	ggt	ctg	gac	gtg	agc	att	432
281	Leu	Gly	Leu	Asn	Ala	Val	Ala	Phe	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Ile	
282			130					135					140				
284	atc	ccg	acc	cag	ggc	gat	gtg	ggt	atc	ggt	agc	acc	gat	gcg	ctg	atg	480
285	Ile	Pro	Thr	Gln	Gly	Asp	Val	Val	Ile	Val	Ser	Thr	Asp	Ala	Leu	Met	
286	145					150					155					160	
288	acc	ggt	ttt	acc	ggc	gat	ttt	gac	tca	gtg	gtc	gac	tgt	aac	aca	tgc	528
289	Thr	Gly	Phe	Thr	Gly	Asp	Phe	Asp	Ser	Val	Val	Asp	Cys	Asn	Thr	Cys	
290				165					170					175			
292	atc	acc	cag	gga	tct	gga	ctg	gta	agc	ttc	gcg	agc	cat	gtg	ccg	tac	576
293	Ile	Thr	Gln	Gly	Ser	Gly	Leu	Val	Ser	Phe	Ala	Ser	His	Val	Pro	Tyr	
294			180						185					190			
296	atc	gag	cag	ggt	atg	caa	ctg	agc	gaa	caa	ttt	aag	cag	aag	agc	ctg	624
297	Ile	Glu	Gln	Gly	Met	Gln	Leu	Ser	Glu	Gln	Phe	Lys	Gln	Lys	Ser	Leu	
298			195					200					205				
300	ggt	ctg	ctg	cag	acc	gcg	acc	aaa	cag	gcg	gag	gcg	gcc	gcc	ccg	gtg	672
301	Gly	Leu	Leu	Gln	Thr	Ala	Thr	Lys	Gln	Ala	Glu	Ala	Ala	Ala	Pro	Val	
302			210					215					220				
304	ggt	ggc	acc	ccg	aaa	agc	cgc	cgt	ccg	gaa	ggt	cgt	gcc	tgg	gcg	caa	720
305	Val	Gly	Thr	Pro	Lys	Ser	Arg	Arg	Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	
306	225					230					235					240	
308	ccg	ggt	acc	atc	atc	ctg	agc	ggt	cgt	ccg	gcg	ggt	gta	ccg	gat	cgt	768
309	Pro	Gly	Thr	Ile	Ile	Leu	Ser	Gly	Arg	Pro	Ala	Val	Val	Pro	Asp	Arg	
310				245					250					255			
312	gaa	gtg	ctg	tat	caa	gaa	ttt	ctc	gag	gcc	tct	aga	gcg	gct	ctc	att	816

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313 Glu Val Leu Tyr Gln Glu Phe Leu Glu Ala Ser Arg Ala Ala Leu Ile
314                               260                               265                               270
316 gaa gag ggg caa cgg ata gcc gag atg ctg aag tcc aag atc cag ggc      864
317 Glu Glu Gly Gln Arg Ile Ala Glu Met Leu Lys Ser Lys Ile Gln Gly
318                               275                               280                               285
320 tta ctg cag caa gcc tcc aag cag gcc caa gac ata aaa atc gac ggt      912
321 Leu Leu Gln Gln Ala Ser Lys Gln Ala Gln Asp Ile Lys Ile Asp Gly
322                               290                               295                               300
324 acc ctg att att ccg aaa gat cgt cgc agc acc ggt aaa agc tgg ggt      960
325 Thr Leu Ile Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly
326 305                               310                               315                               320
328 aaa ccg ggc ttc ctc atc gat agc ttg cat atc aac cag cga gcc gtc      1008
329 Lys Pro Gly Phe Leu Ile Asp Ser Leu His Ile Asn Gln Arg Ala Val
330                               325                               330                               335
332 gtt gca ccg gac aag gag gtc ctt tat gag gct ttt gat gag atg gag      1056
333 Val Ala Pro Asp Lys Glu Val Leu Tyr Glu Ala Phe Asp Glu Met Glu
334                               340                               345                               350
336 ctc gcc atg ggc acc aac ccg aaa ccg gag cgt aaa agc aag cgt aac      1104
337 Leu Ala Met Gly Thr Asn Pro Lys Pro Glu Arg Lys Ser Lys Arg Asn
338                               355                               360                               365
340 acc aac cgt aaa ccg cag gat att aaa ttc ccg ggt agt ggt cag gtg      1152
341 Thr Asn Arg Lys Pro Gln Asp Ile Lys Phe Pro Gly Ser Gly Gln Val
342                               370                               375                               380
344 gtg ggt ggt gtg tac ctg gtg ccg cgt cgt ggt ccg taaggatcc      1197
345 Val Gly Gly Val Tyr Leu Val Pro Arg Arg Gly Pro
346 385                               390                               395
349 <210> SEQ ID NO: 11
350 <211> LENGTH: 396
351 <212> TYPE: PRT
352 <213> ORGANISM: Artificial Sequence
354 <220> FEATURE:
355 <223> OTHER INFORMATION: Amino acid sequence coding for chimeric antigen.
357 <400> SEQUENCE: 11
359 Glu Phe Thr Lys Val Pro Val Ala Tyr Ala Ala Lys Gly Tyr Lys Val
360 1                               5                               10                               15
363 Leu Val Leu Asp Pro Ser Val Ala Ser Thr Leu Gly Phe Gly Ala Tyr
364                               20                               25                               30
367 Leu Ser Lys Ala His Gly Val Asn Pro Asn Ile Arg Thr Gly Ile Arg
368                               35                               40                               45
371 Thr Val Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Tyr
372                               50                               55                               60
375 Leu Ala Asp Gly Gly Cys Ala Gly Gly Ala Tyr Asp Val Ile Gly Ser
376 65                               70                               75                               80
379 Gly Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Val Pro Phe Tyr Gly
380                               85                               90                               95
383 Arg Ala Ile Pro Ile Glu Ala Ile Lys Gly Gly Arg His Leu Val Phe
384                               100                              105                              110
387 Cys His Ser Lys Glu Lys Cys Asp Glu Leu Ala Ser Ala Leu Ser Gly
388                               115                              120                              125

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VERIFICATION SUMMARY

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